



PCT10

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,594A

DATE: 07/16/2002
TIME: 14:58:14

Input Set : A:\5.1198 Sequence Listing.txt
Output Set: N:\CRF3\07162002\J088594A.raw

2 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
W--> 3 <120> TITLE OF INVENTION: Novel Transaldolase
W--> 4 <130> FILE REFERENCE: 00005.001198
W--> 5 <140> CURRENT APPLICATION NUMBER: US/10/088,594A
C--> 6 <141> CURRENT FILING DATE: 2002-06-11
7 <150> PRIOR APPLICATION NUMBER: JP 99/266548
8 <151> PRIOR FILING DATE: 1999-09-21
W--> 9 <160> NUMBER OF SEQ ID: 3
10 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 1080
13 <212> TYPE: DNA
14 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
W--> 15 <400> SEQUENCE: 1
16 atg tct cac att gat gat ctt gca cag ctc ggc act tcc act tgg ctc 48
17 Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu
18 1 5 10 15
19 gac gac ctc tcc cgc gag cgc att act tcc ggc aat ctc agc cag gtt 96
20 Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val
21 20 25 30
22 att gag gaa aag tct gta gtc ggt gtc acc acc aac cca gct att ttc 144
23 Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe
24 35 40 45
25 gca gca gca atg tcc aag ggc gat tcc tac gac gct cag atc gca gag 192
26 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
27 50 55 60
28 ctc aag gcc gct ggc gca tct gtt gac cag gct gtt tac gcc atg agc 240
29 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
30 65 70 75 80
31 atc gac gat gtt cgc aat gct tgt gat ctg ttc acc ggc atc ttc gag 288
32 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
33 85 90 95
34 tcc tcc aac ggc tac gac ggc cgc gtg tcc atc gag gtt gac cca cgt 336
35 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
36 100 105 110
37 atc tct gct gac cgc gac gca acc ctg gct cag gcc aag gag ctg tgg 384
38 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
39 115 120 125
40 gca aag gtt gat cgt cca aac gtc atg atc aag atc cct gca acc cca 432

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41 Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
42 130 135 140
43 ggt tct ttg cca gca atc acc gac gct ttg gct gag ggc atc agc gtt 480
44 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
45 145 150 155 160
46 aac gtc acc ttg atc ttc tcc gtt gct cgc tac cgc gag gtc atc gct 528
47 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala
48 165 170 175
49 gcg tac atc gag gga atc aag cag gca gct gca aac ggc cac gac gta 576
50 Ala Tyr Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
51 180 185 190
52 tcc aag atc cac tct gtg gct tcc ttc gtc tcc cgc gtc gac gtt 624
53 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
54 195 200 205
55 gag atc gac aag cgc ctc gag gca atc gga tcc gat gag gct ttg gct 672
56 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
57 210 215 220
58 ctg cgc ggc aag gca ggc gtt gcc aac gct cag cgc gct tac gct gtg 720
59 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
60 225 230 235 240
61 tac aag gag ctt ttc gac gcc gag ctg cct gaa ggt gcc aac act 768
62 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
63 245 250 255
64 cag cgc cca ctg tgg gca tcc acc ggc gtg aag aac cct gcg tac gct 816
65 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
66 260 265 270
67 gca act ctt tac gtt tcc gag ctg gct ggt cca aac acc gtc aac acc 864
68 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
69 275 280 285
70 atg cca gaa ggc acc atc gac gct gtt ctg gaa ctg ggc aac ctg cac 912
71 Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His
72 290 295 300
73 ggt gac acc ctg tcc aac tcc gcg gca gaa gct gac gct gtg ttc tcc 960
74 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
75 305 310 315 320
76 cag ctt gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg 1008
77 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu
78 325 330 335
79 gag acc gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt 1056
80 Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu
81 340 345 350
E--> 82 gag tcc atg gaa gct cgc ctg aag
83 Glu Ser Met Glu Ala Arg Leu Lys
84 355 360
108 <210> SEQ ID NO: 3
109 <211> LENGTH: 4108
110 <212> TYPE: DNA
111 <213> ORGANISM: Corynebacterium glutamicum ATCC31388
112 <221> NAME/KEY: CDS → insert mandatory <220>

1080 ← insert nucleotide
number at end of
line

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Input Set : A:\5.1198 Sequence Listing.txt
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113 <222> LOCATION: (373)..(2472)
 W--> 114 <221> CDS *met mandaten 2207*
 115 <222> LOCATION: (2643)..(3722)
 E--> 116 <400> SEQUENCE: 3
 117 tcgagagttt gaaggggtcc gattcgttcc gttcgtgacg ctttgtgagg ttttttgacg 60
 118 ttgcaccgt a ttgcgttcc aacattttc ttttccttc gtttttcga gaattttcac 120
 119 ctacaaaagc ccacgtcaca gctcccagac ttaagattgg tcacacccctt gacacattt 180
 120 aaccacagt gttataaaa tgggttcaac atcactatgg ttagagggtgt tgacgggtca 240
 121 gattaagcaa agactactt cgggttagat caccttgcc aaatttgaat caattaacct 300
 122 aagtctgtaa tctgatcatc ggtatctaacg aaaacgaacc aaaacttgg tcccggtta 360
 123 acccaggaag ga atg acc acc ttg acg ctg tca cct gaa ctt cag gcg ctc 411
 124 Met Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu
 125 1 5 10
 126 act gta cgc aat tac ccc tct gat tgg tcc gat gtg gac acc aag gct 459
 127 Thr Val Arg Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala
 128 15 20 25
 129 gta gac act gtt cgt gtc ctc gct gca gac gct gta gaa aac tgt ggc 507
 130 Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly
 131 30 35 40 45
 132 tcc ggc cac cca ggc acc gca atg agc ctg gct ccc ctt gca tac acc 555
 133 Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr
 134 50 55 60
 135 ttg tac cag cgg gtt atg aac gta gat cca cag gac acc aac tgg gca 603
 136 Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala
 137 65 70 75
 138 ggc cgt gac cgc ttc gtt ctt tct tgt ggc cac tcc tct ttg acc cag 651
 139 Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln
 140 80 85 90
 141 tac atc cag ctt tac ttg ggt gga ttc ggc ctt gag atg gat gac ctg 699
 142 Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu
 143 95 100 105
 144 aag gct ctg cgc acc tgg gat tcc ttg acc cca gga cac cct gag tac 747
 145 Lys Ala Leu Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr
 146 110 115 120 125
 147 cgc cac acc aag ggc gtt gag atc acc act ggc cct ctt ggc cag ggt 795
 148 Arg His Thr Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly
 149 130 135 140
 150 ctt gca tct gca gtt ggt atg gcc atg gct gct cgt cgt gag cgt ggc 843
 151 Leu Ala Ser Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly
 152 145 150 155
 153 cta ttc gac cca acc gct gct gag ggc gaa tcc cca ttc gac cac cac 891
 154 Leu Phe Asp Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His
 155 160 165 170
 156 atc tac gtc att gct tct gat ggt gac ctg cag gaa ggt gtc acc tct 939
 157 Ile Tyr Val Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser
 158 175 180 185
 159 gag gca tcc tcc atc gct ggc acc cag cag ctg ggc aac ctc atc gtg 987
 160 Glu Ala Ser Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val
 161 190 195 200 205

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| | | |
|-----|---|------|
| 162 | ttc tgg gat gac aac cgc atc tcc atc gaa gac aac act gag atc gct | 1035 |
| 163 | Phe Trp Asp Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala | |
| 164 | 210 215 220 | |
| 165 | ttc aac gag gac gtt gtt gct cgt tac aag gct tac ggc tgg cag acc | 1083 |
| 166 | Phe Asn Glu Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr | |
| 167 | 225 230 235 | |
| 168 | att gag gtt gag gct ggc gag gac gtt gca gca atc gaa gct gca gtg | 1131 |
| 169 | Ile Glu Val Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val | |
| 170 | 240 245 250 | |
| 171 | gct gag gct aag aag gac acc aag cga cct acc ttc atc cgc gtt cgc | 1179 |
| 172 | Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg | |
| 173 | 255 260 265 | |
| 174 | acc atc atc ggc ttc cca gct cca acc atg atg aac acc ggt gct gtg | 1227 |
| 175 | Thr Ile Ile Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val | |
| 176 | 270 275 280 285 | |
| 177 | cac ggt gct gct ctt ggc gca gct gag gtt gca gca acc aag act gag | 1275 |
| 178 | His Gly Ala Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu | |
| 179 | 290 295 300 | |
| 180 | ctt gga ttc gat cct gag gct cac ttc gcg atc gac gat gag gtt atc | 1323 |
| 181 | Leu Gly Phe Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile | |
| 182 | 305 310 315 | |
| 183 | gct cac acc cgc tcc gca gag cgc gct gca cag aag aag gct gca | 1371 |
| 184 | Ala His Thr Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala | |
| 185 | 320 325 330 | |
| 186 | tgg cag gtc aag ttc gat gag tgg gca gct gcc aac cct gag aac aag | 1419 |
| 187 | Trp Gln Val Lys Phe Asp Glu Trp Ala Ala Asn Pro Glu Asn Lys | |
| 188 | 335 340 345 | |
| 189 | gct ctg ttc gat cgc ctg aac tcc cgt gag ctt cca gcg ggc tac gct | 1467 |
| 190 | Ala Leu Phe Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala | |
| 191 | 350 355 360 365 | |
| 192 | gac gag ctc cca aca tgg gat gca gat gag aag ggc gtc gca act cgt | 1515 |
| 193 | Asp Glu Leu Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg | |
| 194 | 370 375 380 | |
| 195 | aag gct tcc gag gct gca ctt cag gca ctg ggc aag acc ctt cct gag | 1563 |
| 196 | Lys Ala Ser Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu | |
| 197 | 385 390 395 | |
| 198 | ctg tgg ggc ggt tcc gct gac ctc gca ggt tcc aac aac acc gtg atc | 1611 |
| 199 | Leu Trp Gly Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile | |
| 200 | 400 405 410 | |
| 201 | aag ggc tcc cct tcc ttc ggc cct gag tcc atc tcc acc gag acc tgg | 1659 |
| 202 | Lys Gly Ser Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp | |
| 203 | 415 420 425 | |
| 204 | tct gct gag cct tac ggc cgt aac ctg cac ttc ggt atc cgt gag cac | 1707 |
| 205 | Ser Ala Glu Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His | |
| 206 | 430 435 440 445 | |
| 207 | gct atg gga tcc atc ctc aac ggc att tcc ctc cac ggt ggc acc cgc | 1755 |
| 208 | Ala Met Gly Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg | |
| 209 | 450 455 460 | |
| 210 | cca tac ggt gga acc ttc ctc atc ttc tcc gac tac atg cgt cct gca | 1803 |

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| | | | | | | | | | | | | | | | | | |
|-----|-------------|------------|------------|-------------|------------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 211 | Pro | Tyr | Gly | Gly | Thr | Phe | Leu | Ile | Phe | Ser | Asp | Tyr | Met | Arg | Pro | Ala | |
| 212 | | | | | 465 | | | | 470 | | | | 475 | | | | |
| 213 | gtt | cgt | ctt | gcá | gct | ctc | atg | gag | acc | gac | gct | tac | tac | gtc | tgg | acc | |
| 214 | Val | Arg | Leu | Ala | Ala | Leu | Met | Glu | Thr | Asp | Ala | Tyr | Tyr | Val | Trp | Thr | |
| 215 | | | | | | | 480 | | 485 | | | | 490 | | | | |
| 216 | cac | gac | tcc | atc | ggt | ctg | ggc | gaa | gat | ggc | cca | acc | cac | cag | cct | gtt | |
| 217 | His | Asp | Ser | Ile | Gly | Leu | Gly | Glu | Asp | Gly | Pro | Thr | His | Gln | Pro | Val | |
| 218 | | | | | | | 495 | | 500 | | | 505 | | | | | |
| 219 | gaa | acc | ttg | gct | gcg | ctg | cgc | gcc | atc | cca | ggt | ctg | tcc | gtc | ctg | cgt | |
| 220 | Glu | Thr | Leu | Ala | Ala | Leu | Arg | Ala | Ile | Pro | Gly | Leu | Ser | Val | Leu | Arg | |
| 221 | 510 | | | | | | 515 | | | | 520 | | | 525 | | | |
| 222 | cct | gca | gat | gcg | aat | gag | acc | gcc | cag | gct | tgg | gct | gca | gca | ctt | gag | |
| 223 | Pro | Ala | Asp | Ala | Asn | Glu | Thr | Ala | Gln | Ala | Trp | Ala | Ala | Ala | Leu | Glu | |
| 224 | | | | | | | 530 | | | 535 | | | 540 | | | | |
| 225 | tac | aag | gaa | ggc | cct | aag | ggt | ctt | gca | ctg | acc | cgc | cag | aac | gtt | cct | |
| 226 | Tyr | Lys | Glu | Gly | Pro | Lys | Gly | Leu | Ala | Leu | Thr | Arg | Gln | Asn | Val | Pro | |
| 227 | | | | | | | 545 | | | 550 | | | 555 | | | | |
| 228 | gtt | ctg | gaa | ggc | acc | aag | gag | aag | gct | gct | gaa | ggc | gtt | cgc | cgc | ggt | |
| 229 | Val | Leu | Glu | Gly | Thr | Lys | Glu | Lys | Ala | Ala | Glu | Gly | Val | Arg | Arg | Gly | |
| 230 | | | | | | | 560 | | | 565 | | | 570 | | | | |
| 231 | ggc | tac | gtc | ctg | gtt | gag | ggt | tcc | aag | gaa | acc | cca | gat | gtg | atc | ctc | |
| 232 | Gly | Tyr | Val | Leu | Val | Glu | Gly | Ser | Lys | Glu | Thr | Pro | Asp | Val | Ile | Leu | |
| 233 | | | | | | | 575 | | | 580 | | | 585 | | | | |
| 234 | atg | ggc | tcc | ggc | tcc | gag | gtt | cag | ctt | gca | gtt | aac | gct | gcg | aaa | gct | |
| 235 | Met | Gly | Ser | Gly | Ser | Glu | Val | Gln | Leu | Ala | Val | Asn | Ala | Ala | Lys | Ala | |
| 236 | 590 | | | | | | 595 | | | | 600 | | | 605 | | | |
| 237 | ctg | gaa | gct | gag | ggc | gtt | gca | gct | cgc | gtt | gtt | tca | gtt | cct | tgc | atg | |
| 238 | Leu | Glu | Ala | Glu | Gly | Val | Ala | Ala | Arg | Val | Val | Ser | Val | Pro | Cys | Met | |
| 239 | | | | | | | 610 | | | 615 | | | 620 | | | | |
| 240 | gat | tgg | ttc | cag | gag | cag | gac | gca | gag | tac | atc | gag | tcc | gtt | ctg | cct | |
| 241 | Asp | Trp | Phe | Gln | Glu | Gln | Asp | Ala | Glu | Tyr | Ile | Glu | Ser | Val | Leu | Pro | |
| 242 | | | | | | | 625 | | | 630 | | | 635 | | | | |
| 243 | gca | gct | gtg | acc | gct | cgt | gtg | tct | gtt | gaa | gct | ggc | atc | gca | atg | cct | |
| 244 | Ala | Ala | Val | Thr | Ala | Arg | Val | Ser | Val | Glu | Ala | Gly | Ile | Ala | Met | Pro | |
| 245 | | | | | | | 640 | | | 645 | | | 650 | | | | |
| 246 | tgg | tac | cgc | ttc | ttg | ggc | acc | cag | ggc | cgt | gct | gtc | tcc | ctt | gag | cac | |
| 247 | Trp | Tyr | Arg | Phe | Leu | Gly | Thr | Gln | Gly | Arg | Ala | Val | Ser | Leu | Glu | His | |
| 248 | | | | | | | 655 | | | 660 | | | 665 | | | | |
| 249 | ttc | ggt | gct | tct | gcg | gat | tac | cag | acc | ctg | ttt | gag | aag | ttc | ggc | atc | |
| 250 | Phe | Gly | Ala | Ser | Ala | Asp | Tyr | Gln | Thr | Leu | Phe | Glu | Lys | Phe | Gly | Ile | |
| 251 | 670 | | | | | | 675 | | | | 680 | | | 685 | | | |
| 252 | acc | acc | gat | gca | gtc | gtg | gca | gcg | gcc | aag | gac | tcc | att | aac | agt | | |
| 253 | Thr | Thr | Asp | Ala | Val | Val | Ala | Ala | Ala | Lys | Asp | Ser | Ile | Asn | Ser | | |
| 254 | | | | | | | 690 | | | 695 | | | 700 | | | | |
| 255 | taattggccct | gctgtttta | gcttcaaccc | ggggcagttat | gattctccgg | aatttttattt | g | | | | | | | | | | 2532 |
| 256 | ccccgggttg | ttgttgttaa | tcggtacaaa | gggtcttaag | cacatccctt | acttgcctgc | | | | | | | | | | | 2592 |
| 257 | tctccttgag | cacagttcaa | gaacaattct | tttaaggaaa | attagtttc | atg | tct | | | | | | | | | | 2648 |
| 258 | | | | | | | | | | | | | | | Met | Ser | |

W--> 259

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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|
| 260 | cac | att | gat | gat | ctt | gca | cag | ctc | ggc | act | tcc | act | tgg | ctc | gac | gac | 2696 |
| 261 | His | Ile | Asp | Asp | Leu | Ala | Gln | Leu | Gly | Thr | Ser | Thr | Trp | Leu | Asp | Asp | |
| 262 | | | | | 5 | | | | 10 | | | | | 15 | | | |
| 263 | ctc | tcc | cgc | gag | cgc | att | act | tcc | ggc | aat | ctc | agc | cag | gtt | att | gag | 2744 |
| 264 | Leu | Ser | Arg | Glu | Arg | Ile | Thr | Ser | Gly | Asn | Leu | Ser | Gln | Val | Ile | Glu | |
| 265 | | | | | | 20 | | | 25 | | | | 30 | | | | |
| 266 | gaa | aag | tct | gta | gtc | ggt | gtc | acc | acc | aac | cca | gct | att | ttc | gca | gca | 2792 |
| 267 | Glu | Lys | Ser | Val | Val | Gly | Val | Thr | Thr | Asn | Pro | Ala | Ile | Phe | Ala | Ala | |
| 268 | | | | | | 35 | | | 40 | | | 45 | | 50 | | | |
| 269 | gca | atg | tcc | aag | ggc | gat | tcc | tac | gac | gct | cag | atc | gca | gag | ctc | aag | 2840 |
| 270 | Ala | Met | Ser | Lys | Gly | Asp | Ser | Tyr | Asp | Ala | Gln | Ile | Ala | Glu | Leu | Lys | |
| 271 | | | | | | 55 | | | | 60 | | | 65 | | | | |
| 272 | gcc | gct | ggc | gca | tct | gtt | gac | cag | gct | gtt | tac | gcc | atg | agc | atc | gac | 2888 |
| 273 | Ala | Ala | Gly | Ala | Ser | Val | Asp | Gln | Ala | Val | Tyr | Ala | Met | Ser | Ile | Asp | |
| 274 | | | | | | 70 | | | 75 | | | 80 | | | | | |
| 275 | gat | gtt | cgc | aat | gct | tgt | gat | ctg | ttc | acc | ggc | atc | ttc | gag | tcc | tcc | 2936 |
| 276 | Asp | Val | Arg | Asn | Ala | Cys | Asp | Leu | Phe | Thr | Gly | Ile | Phe | Glu | Ser | Ser | |
| 277 | | | | | | 85 | | | 90 | | | 95 | | | | | |
| 278 | aac | ggc | tac | gac | ggc | cgc | gtg | tcc | atc | gag | gtt | gac | cca | cgt | atc | tct | 2984 |
| 279 | Asn | Gly | Tyr | Asp | Gly | Arg | Val | Ser | Ile | Glu | Val | Asp | Pro | Arg | Ile | Ser | |
| 280 | | | | | | 100 | | | 105 | | | 110 | | | | | |
| 281 | gct | gac | cgc | gac | gca | acc | ctg | gct | cag | gcc | aag | gag | ctg | tgg | gca | aag | 3032 |
| 282 | Ala | Asp | Arg | Asp | Ala | Thr | Leu | Ala | Gln | Ala | Lys | Glu | Leu | Trp | Ala | Lys | |
| 283 | | | | | | 115 | | | 120 | | | 125 | | 130 | | | |
| 284 | gtt | gat | cgt | cca | aac | gtc | atg | atc | aag | atc | cct | gca | acc | cca | ggt | tct | 3080 |
| 285 | Val | Asp | Arg | Pro | Asn | Val | Met | Ile | Lys | Ile | Pro | Ala | Thr | Pro | Gly | Ser | |
| 286 | | | | | | 135 | | | | 140 | | | 145 | | | | |
| 287 | ttg | cca | gca | atc | acc | gac | gct | ttg | gct | gag | ggc | atc | agc | gtt | aac | gtc | 3128 |
| 288 | Leu | Pro | Ala | Ile | Thr | Asp | Ala | Leu | Ala | Glu | Gly | Ile | Ser | Val | Asn | Val | |
| 289 | | | | | | 150 | | | 155 | | | 160 | | | | | |
| 290 | acc | ttg | atc | ttc | tcc | gtt | gct | cgc | tac | cgc | gag | gtc | atc | gct | gcg | tac | 3176 |
| 291 | Thr | Leu | Ile | Phe | Ser | Val | Ala | Arg | Tyr | Arg | Glu | Val | Ile | Ala | Ala | Tyr | |
| 292 | | | | | | 165 | | | 170 | | | 175 | | | | | |
| 293 | atc | gag | gga | atc | aag | cag | gca | gct | gca | aac | ggc | cac | gac | gta | tcc | aag | 3224 |
| 294 | Ile | Glu | Gly | Ile | Lys | Gln | Ala | Ala | Ala | Asn | Gly | His | Asp | Val | Ser | Lys | |
| 295 | | | | | | 180 | | | 185 | | | 190 | | | | | |
| 296 | atc | cac | tct | gtg | gct | tcc | ttc | gtc | tcc | cgc | gtc | gac | gtt | gag | atc | 3272 | |
| 297 | Ile | His | Ser | Val | Ala | Ser | Phe | Phe | Val | Ser | Arg | Val | Asp | Val | Glu | Ile | |
| 298 | | | | | | 195 | | | 200 | | | 205 | | 210 | | | |
| 299 | gac | aag | cgc | ctc | gag | gca | atc | gga | tcc | gat | gag | gct | ttg | gct | ctg | cgc | 3320 |
| 300 | Asp | Lys | Arg | Leu | Glu | Ala | Ile | Gly | Ser | Asp | Glu | Ala | Leu | Ala | Leu | Arg | |
| 301 | | | | | | 215 | | | | 220 | | | 225 | | | | |
| 302 | ggc | aag | gca | ggc | gtt | gcc | aac | gct | cag | cgc | gct | tac | gct | gtg | tac | aag | 3368 |
| 303 | Gly | Lys | Ala | Gly | Val | Ala | Asn | Ala | Gln | Arg | Ala | Tyr | Ala | Val | Tyr | Lys | |
| 304 | | | | | | 230 | | | | 235 | | | 240 | | | | |
| 305 | gag | ctt | ttc | gac | gcc | gag | ctg | cct | gaa | ggt | gcc | aac | act | cag | cgc | | 3416 |
| 306 | Glu | Leu | Phe | Asp | Ala | Ala | Glu | Leu | Pro | Glu | Gly | Ala | Asn | Thr | Gln | Arg | |
| 307 | | | | | | 245 | | | 250 | | | 255 | | | | | |
| 308 | cca | ctg | tgg | qca | tcc | acc | ggc | gtg | aag | aac | cct | gcg | tac | gct | gca | act | 3464 |

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,594A

DATE: 07/16/2002
TIME: 14:58:14

Input Set : A:\5.1198 Sequence Listing.txt
Output Set: N:\CRF3\07162002\J088594A.raw

309 Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr
310 260 265 270
311 ctt tac gtt tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca 3512
312 Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro
313 275 280 285 290
314 gaa ggc acc atc gac gct gtt ctg gaa ctg ggc aac ctg cac ggt gac 3560
315 Glu Gly Thr Ile Asp Ala Val Leu Glu Leu Gly Asn Leu His Gly Asp
316 295 300 305
317 acc ctg tcc aac tcc gcg gca gaa gct gac gct gtc ttc tcc cag ctt 3608
318 Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu
319 310 315 320
320 gag gct ctg ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc 3656
321 Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr
322 325 330 335
323 gag ggt gtg gac aag ttt gtt gct tct tgg agc gaa ctg ctt gag tcc 3704
324 Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser
325 340 345 350
326 atg gaa gct cgc ctg aag tagaatcagc acgctgcatac agtaacggcg 3752
327 Met Glu Ala Arg Leu Lys
328 355 360
329 acatgaaatc gaatttagttc gatcttatgt ggccgttaca catctttcat taaaagaaagg 3812
330 atcgtgacgc taccatctgt agcacaaaca cgacccctc cagctggaca aaccactgc 3872
331 gcgacccgca ggataaacga ctcccccgca tcgctggccc ttccggcatg gtatcttcg 3932
332 gtgtcaactgg cgacttggct cgaaggaagc tgctccccgc catttatgt ctagcaaacc 3992
333 gcggattgct gccccagga ttctcggttgg tagttacgg ccgcccgcgaa tggccaaag 4052
334 aagactttga aaaatacgtc cgcgtatgcg caagtgtgg tgctcgtaacg gaattc 4108

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/088,594A

DATE: 07/16/2002
TIME: 14:58:15

Input Set : A:\5.1198 Sequence Listing.txt
Output Set: N:\CRF3\07162002\J088594A.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:283 W: Missing Blank Line separator, <140> field identifier
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <210> field identifier
L:15 M:283 W: Missing Blank Line separator, <400> field identifier
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1080 SEQ:1
L:89 M:283 W: Missing Blank Line separator, <400> field identifier
L:114 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:116 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:3
L:116 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3